AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

1. (original): A protein comprising:

a) 4-α-helix bundle motif formed from the α-helices of ROP (repressor of primer) and

b) a redox centre.

2. (currently amended): The protein of Claim 1, wherein the redox centre ~~is a metal, preferably iron or cooper, is an iron-sulphur centre, haem, FMN or FAD and is preferably haem~~comprises a metal atom which is stable in two different oxidation states.

3. (currently amended): The protein of Claim 1~~ or 2~~, wherein the redox centre is bound to the protein, ~~preferably coordinated~~by coordination by one or more of histidine, leucine, methionine or cysteine residues~~ and more preferably by 2 histidine residues~~.

4. (currently amended): The protein of Claim 1~~ or 2~~, wherein the redox centre is covalently bound to the protein.

5. (original): The protein of Claim 1 which has a redox mid-point potential in the range of -485 to +320mV.

6. (currently amended): The protein of Claim 1 which has α-helix regions each having at least 60%~~, preferably 70% and more preferably 80%~~ similarity or identity with the α-helix regions of sequence ID Nos. 1 and 3.

7. (original): The protein of claim 6, wherein said four α-helix regions are connected by loops.

8. (original): The protein of claim 7, wherein the four α-helices are joined in the order 1-1'-2'-2.

9. (currently amended): The protein of Claim 1 which is formed by connecting two wild type ROP proteins to obtain the 4-helix bundle as one continuous polypeptide having at least 60%~~, preferably 70% and more preferably 80%~~ similarity or identity with sequence ID No. 8.

10. (original): The protein of claim 9, wherein the histidine residues corresponding to H76, H78, H107 and H109 in sequence ID No. 8 are removed.

11. (currently amended): The protein of claim 9~~ or 10~~, wherein histidine, leucine, methionine or cystein residues are introduced one or both positions corresponding to 56 and 113 in sequence ID No. 8~~, preferably histidines are introduced at both positions 56 and 113~~.

12. (currently amended): The protein of ~~any preceeding claim~~claim 1 which has a haem redox centre coordinated to the 4-α-helix bundle motif via two histidine residues.

13. (original): The protein of claim 12 which has a mid-point potential in the range -400mV to +300MV.

14. (original): The protein of claim 12 which has the sequence as indicated by sequence ID No. 11.

15. (currently amended): The protein of ~~any one of claims 1 to 14~~claim 1 which has a stability, measured as the unfolding free energy when denaturant is added to the protein, of $\Delta G_{obs}H_2O\geq$ wherein $y\geq 3.0$ kcal/mol.

16. (currently amended): A method of producing the protein of ~~any one of claims 1 to 15~~claim 1 comprising

i) expressing all four α-helices as a single polypeptide chain;

ii) engineering the required mutations to enable redox centre binding;

iii) expressing and purifying, or producing the redox centre binding mutant; and

iv) ~~Incubating~~ incubating the ~~protein~~ mutant with an excess of the redox centre to produce the protein.

17. (currently amended): A nucleotide sequence which encodes the protein of ~~any one of claims 1 to 15~~claim 1 or a fragment thereof.

18. (original): A vector comprising the nucleotide sequence of claim 17.

19. (canceled).

20. (currently amended): A method of passing electrons along a sequence of electron carriers, in which each electron carrier is reduced and then oxidized or vice versa by electron movement and the sequence of electron carriers includes the protein of ~~any one of claims 1 to 15~~claim 1.

21. (currently amended): An apparatus comprising the protein of ~~any one of claims 1 to 15~~claim 1 associated with an electrode.

22. (original): An apparatus according to claim 21 wherein the protein is absorbed onto an electrode.

23. (new): A protein according to claim 2 in which the redox centre is an iron sulfur centre.

24. (new): A protein according to claim 1 in which the redox centre does not contain a metal atom.

25. (new): A protein according to claim 24 in which the redox centre is FMN or FAD.

26. (new): A protein according to claim 6 in which the α-helix regions each have at least 80% similarity or identity with the α-helix regions of sequence ID No. 1.

27. (new): A protein according to claim 9 in which the continuous polypeptide has at least 80% similarity or identity with sequence ID No. 8.